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INSTITUT NATIONAL DE LA SANTE ET DE LA  
RECHERCHE MEDICALE (INSERM)  
101, rue de Tolbiac  
75654 Paris Cédex 13  
FRANCE

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A vaccine composition comprising an immunoadjuvant compound consisting of a RHO  
GTPase family activator

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### **Field of the invention**

The present invention relates to a vaccine composition comprising an immuno adjuvant compound, wherein said immuno adjuvant  
5 compound consists of a RHO GTPase family activator.

### **Background of the invention**

Vaccines have proven to be successful, highly acceptable  
10 methods for the prevention of infectious diseases. There are cost effective, and do not induce antibiotic resistance to the target pathogen or affect normal flora present in the host. In many cases, such as when inducing anti-viral immunity, vaccines can prevent a disease for which there are no viable curative or ameliorative treatments available.

Vaccines function by triggering the immune system to induce a  
15 response to an agent, or an antigen, typically in an infectious organism or a portion thereof that is introduced into the body in a non-infectious or non-pathogenic form.

Once the immune system has been "primed" or sensitised to the  
20 organism, later exposure of the immune system to this organism, results in a rapid and robust immune response that destroys the pathogen before it can multiply or infect enough cells in the host organism to cause disease symptoms.

The agent, or antigen, used to prime the immune system can be  
25 the entire organism in a less infectious state, known as an attenuated organism, or in some cases, component of the organism such as carbohydrate proteins or peptides representing various structural components of the organism.

In many cases, it is necessary to enhance the immune response  
30 to the antigens present in a vaccine in order to stimulate the immune system to a sufficient extent to make a vaccine effective, i.e., to confer immunity. Many proteins and most peptide and carbohydrate antigens, administered alone, do not elicit a sufficient antibody response to confer immunity. Such antigens need to be presented to the immune system in such a way that they will be recognized as foreign and will elicit an  
35 immune response.

To this end, additives like adjuvants, have been devised, which immobilise antigens and stimulate the immune response.

Recombinant proteins are promising vaccine or immunogenic composition candidates because they can be produced at high yield and purity and manipulated to maximize desirable activities and minimize undesirable ones.

However, because they can be poorly immunogenic, methods to enhance the immune response to recombinant proteins are important in the development of vaccines or immunogenic compositions. Such antigens, especially when recombinantly produced, may elicit a stronger response when administered in conjunction with an adjuvant.

The best known adjuvant, Freund's complete adjuvant, consists of a mixture of mycobacteria in an oil/water emulsion.

Freund's adjuvant works in two ways; first, by enhancing cell and humoral-mediated immunity, and second by blocking rapid dispersal of the antigens challenge, also called "depot effect". However, due to frequent toxic physiological and immunological reactions to this material, Freund's adjuvant cannot be used in humans.

Another molecule that has been shown to have stimulatory or adjuvant activity is endotoxin, although known as lipopolysaccharide (LPS).

LPS stimulates the immune system by triggering an immediate immune response, a response that has evolved to enable an organism to recognize endotoxin and the invading bacteria (of which it is a component) without the need for the organism to have been previously exposed. But LPS is although too toxic to be a viable adjuvant.

Thus, there is a recognized and permanent need in the art for new compounds which can be administered with antigens in order to stimulate the immune system and generate a more robust antibody response to the antigen than will be seen if the antigens were injected alone.

Additionally, it should be noted that parenteral administration i.e. intramuscularly or sub-cutaneous, of antigens of vaccines are normally regarded as the most convenient way of administration.

However, the injection presents a range of disadvantages. It requires the use of sterile syringes and may cause pains and irritations,

particularly in the case of repeated injections, including the risk of infection. More significantly, intramuscularly injections are often poorly tolerated. There is often likely to be indurations (hardening of tissue) haemorrhages and/or necrosis (local death of tissue) at the injection site.

5 Besides, untrained person cannot administer injections.

Based on these observations, it should be noted that mucosal immunity has take a considerable importance in vaccine development because nearly all viral, bacterial and parasitic agent that cause disease of the intestinal, respiratory and genital tracks enter through the mucosal  
10 barrier. Furthermore, mucosal and systemic immune responses are often elicited and regulated independently, and induction of protective immunity at the most frequent sites of entry is likely to be most effective. Additionally, young children and elderly individuals may respond better to mucosal vaccines because the mucosal immune system develops earlier  
15 and appears to remain functional longer than the systemic compartment. Mucosal immunisations are also easier and less expensive than systemic immunisations. For example, the existence of an oral polio vaccine has allowed immunisation campaigns that may soon eradicate polio worldwide.

20 Accordingly, it is also an object of the present invention to provide a vaccine composition comprising an immunoadjuvant compound which could be administered by the mucosal route. These and further objects will be apparent to one ordinary skill in the art.

#### 25 **Summary of the invention**

The present invention is based on the experimental findings that an activator of Rho GTPases, namely the cytotoxic necrotizing factor 1 (cnf1) bears immunostimulatory properties towards the systemic and mucosal responses to orally administered ovalbumine, a prototype  
30 soluble protein antigen. CNF1 consists of an injection domain (amino acid residues 1-719 of SEQ ID N°1), allowing the binding and endosomal penetration of the toxin, followed by the intracytoplasmic injection of its catalytic domain (amino acid residues 720-1014 of SEQ ID N°1), responsible for Rho GTPases protein family activation.



A first object of the invention consists in a vaccine composition comprising an immunoadjuvant compound, wherein said immunoadjuvant compound consists of a Rho GTPase activator.

In another aspect, the invention relates to a vaccine composition wherein said immunoadjuvant compound is selected from the group consisting of :

- a polypeptide comprising the amino acid sequence starting at the amino acid residue 720 and ending at the amino acid residue 1014 of sequence SEQ ID N°1,
- 10 - a polypeptide comprising the amino acid sequence starting at the amino acid residue 720 and ending at the amino acid residue 1014 of sequence SEQ ID N°2,
- a polypeptide comprising the amino acid sequence starting at the amino acid residue 720 and ending at the amino acid residue 1014 of sequence SEQ ID N°3,
- 15 - a polypeptide comprising the amino acid sequence starting at the amino acid residue 1146 and ending at the amino acid residue 1451 of sequence SEQ ID N°4,
- a polypeptide comprising the amino acid sequence SEQ ID N°5,
- 20 - a polypeptide comprising the amino acid sequence SEQ ID N°6,
- a polypeptide comprising the amino acid sequence SEQ ID N°7,
- a polypeptide comprising the amino acid sequence SEQ ID N°8, and
- a polypeptide comprising the amino acid sequence SEQ ID N°9.

The present invention also relates to a vaccine composition wherein the immunoadjuvant compound is a protein comprising a polypeptide consisting of; from the N-terminal end to the C-terminal end, respectively:

- a) the injection domain of a Rho GTPase activator , and
- b) the catalytic domain of a Rho GTPase activator.

### 30 **Description of drawings**

#### **Figure 1: CNF1 effects on cell signaling pathway.**

- 1A : Immunoblots showing the kinetics of CNF1-induced activation of
- 35 Rho, Rac and Cdc42 in contrast to Ras, in HUVEC. Cells were

treated with  $10^{-9}$ M CNF1 for different periods of time. Cell lysates were subjected to GST-fusion protein pull-down assays (noted GTPases-GTP). In parallel, 2% of each cell lysate were processed for immunoblotting to monitor their cellular depletion (noted Total-GTPases).

- 1B : Quantification of the CNF1-induced Rho protein activation. Immunoblots were scanned and quantified using N.I.H. Image 1.6. The level of activated Rho proteins was compared to the total Rho GTPase level present in 2% of control cell lysates (mean value of three independent experiments  $\pm$  SD).
- 1C : Immunoblots showing the interference of native CNF1 and catalytic inactive CNF1-C866S on cell signaling. HUVEC were treated with " $10^{-9}$ M" CNF1 or CNF1-C866S for the indicated periods of time, prior to immunoblotting analysis. MAP kinase signaling was investigated using anti-phosphop44/42 MAP Kinase (noted P-p44/42) and anti-phospho-p38 MAP Kinase (noted P-p38) antibodies. Jun kinase activity was investigated by anti-phospho-c-jun (noted P-c-jun) immunoblotting. NF-kappaB signaling pathway activation was investigated by following the I $\kappa$ B $\alpha$  cellular depletion on immunoblots.

## **Figure 2 : Immunoadjuvant properties of orally administered CNF1**

- 2A : Serum IgG antibody responses to orally co-administrated ovalbumin (OVA) and toxins. Five groups of mice were fed OVA alone or co-administrated with either CT (10 $\mu$ g), CNF1 (1 $\mu$ g or 10 $\mu$ g) or CNF1-C866S (10 $\mu$ g). Groups of eight mice were immunized with CNF1 or CNF1-C866S, whereas groups of four mice were immunized with OVA alone or CT. Groups of mice were challenged once, two weeks after the first immunization and sera collected 30 days after the first immunization. Data are expressed as geometric mean serum IgG anti-OVA Ab titers and individual titers are indicated (full circle). These results are representative of three independent experiments.

- 2B : IgG-subclasses distribution of serum anti-OVA antibody responses after oral immunization with OVA and native or mutated CNF1 (CNF1-C866S). Groups of 8 mice were challenged twice after the first immunization and sera collected 45 days after the first immunization. Levels of the anti-OVA Ig-subclasses are expressed as a geometric mean (histogram).  
5
- 2C: Feeding CNF1 promotes intestinal antibody responses to co-administered OVA. Groups of 8 mice were immunized three times orally with OVA and either CNF1 or CNF1-C866S. Intestinal IgA antibody responses were determined by the PERFEXT method (Villavedra et al., 1997). Data are expressed as geometric mean IgA antibody titer (histogram).  
10
- 15 **Figure 3 Measure of the immunoadjuvant properties and toxin activity of CNF1 and DNT.**
  - 3A: Measure of the toxin activity of CNF1, CNF1-CTER (720-1014), DNT-CTER (1154-1451) estimated by HEp-2 cells multinucleation assay, as previously described (Lemichez et al., 1997). As previously reported, CNF1-CTER is poorly active on cells due to its inability to penetrate into the cytosol (Lemichez et al., 1997). DNT-CTER shows a one thousand lower activity, as compared to CNF1.  
20
  - 3B: Serum IgG antibody responses to orally co-administered ovalbumin (OVA) and DNT or CNF1-toxin catalytic domains. Groups of 4 mice were fed OVA alone or co-administered with either CNF1-CTER (720-1014) (100µg) or DNT-CTER (1154-1451) (100µg). For CNF1, a group of height mice were fed OVA and CNF1 (10µg). Mice were challenged once, two weeks after the first immunization and sera collected 30 days after the first immunization. Data are expressed as geometric mean serum IgG anti-OVA Ab titers.  
25  
30

## **DETAILED DESCRIPTION OF THE INVENTION**

The inventors have found according to the invention that Rho GTPase activators bear immunoadjuvant properties *in vivo*, when co-administered with an antigen, like ovalbumin.

Rho proteins are essential regulatory molecules controlling the actin cytoskeleton organisation and dynamics to accomplish different tasks such as cell polarity, movement, differentiation and phagocytosis (Takai et al., 2001, Etienne-Manneville et al., 2002, Chimini and Chavrier, (2000)). Importance of Rho proteins in physiology is also evidenced by their direct or indirect implication as part of signaling molecules found mutated in human genetic disorders, as well as targets of numerous bacterial virulence factors and toxins (Boettner and Van Aelst, (2002) Boquet and Lemichez, (2003).

Rho proteins interfere with a large variety of signaling pathways controlling gene transcription (Bishop et al., 2000). Among them, a recent report has evidenced the activation of Rac and Cdc42 downstream the Toll-like receptor 2, a gram positive pathogen molecular pattern recognition receptor (PAMP) (Arbibe et al. (2000), Medzhitov et al. (2002).

Also exemplifying the inter-relation between Rho proteins and the host defences is the Rac, Cdc42, VAV and WASP formation of a supra-molecular activation complex (SMAC or "immunological synapse" crucial for lymphocyte activation (Krawczyk et al. 2001).

Many different pathogenic bacteria have evolved virulence factors and toxins aimed at mimicking an activation of Rho GTPase protein family, naturally occurring in eukaryotic cells via specific regulators namely GEF (for guanine nucleotide exchange factors). These cellular GEF consist in domains comprised in large proteins as best described for DbI (Olson et al., 1996; Schmidt and Hall 2002). Despite their lack of sequence homologies, virulence factors of pathogenic bacteria, for instance SopE and SopE2 from *Salmonella* have a GEF-like activity (Galan et al., 2000). Some other known factors of pathogenic bacteria, namely IpaC from *Shigella* and CagA from *Helicobacter*, activate Rho GTPases by yet uncharacterised molecular mechanisms (Tran Van

Nhieu et al., 2000; Boquet and Lemichez 2003). Finally, a group of bacterial toxins comprising CNF1 also activates Rho proteins through a post-traductional modification (Boquet and Lemichez 2003)

According to the invention, the inventors have now surprisingly found that the cytotoxic necrotising factor 1 (CNF1), has immunoadjuvant properties. More precisely, the inventors have found that CNF1 bears immunostimulatory properties toward the systemic and mucosal responses to orally administrated ovalbumin in mice.

Additionally, the inventors have found that a mutant of CNF1, namely CNF1-C866S, a catalytically inactive mutant of CNF1 toward GTPases, in contrast to the wild type toxin, does not stimulate the systemic and mucosal responses to ovalbumin. This result points for Rho GTPases proteins activation being directly involved in the immunostimulatory effects of CNF1.

Supporting this point, the inventors have also found according to the invention that the catalytic domain of CNF1, and the catalytic domain of DNT, another Rho GTPase activator, bear also immunoadjuvant properties *in vivo*, when co-administered with an antigen, like ovalbumin.

Taken together, these results demonstrate clearly that different Rho GTPases activators, structurally different, have immunoadjuvant properties.

Furthermore, the inventors have found that non neutralizing anti-CNF1 antibodies are naturally found in humans, and that CNF1 activates the Rho GTPase proteins only transiently. Taken together these results demonstrate that CNF1 can be used as an immunoadjuvant compound, devoid of adverse effects such as the toxic effects described for LPS or Cholera Toxin B.

Accordingly, a first object of the invention consists in a vaccine composition comprising an immunoadjuvant compound, wherein said immunoadjuvant compound consists of a Rho.GTPase activator.

By "immunoadjuvant" it is herein intended a substance enhancing the immunogenicity of an antigen. By "Rho GTPase activator" it is intended herein a compound, which maintains Rho GTPases in a form bound to GTP. By "Rho GTPases", the one skilled in the art will understand the proteins belonging to the Rho GTPase family, which

encompasses RhoA, RhoB, RhoC, Rac1, Rac2 and Cdc42. (Burridge and Wennerberg, 2004).

5 The level of Rho GTPase bound to GTP can be easily measured by the methods, referred by those skilled in the art as GST-pull down assays and described for RhoA, B and C by Ren et al., 1999 and for Rac1, Rac2 and Cdc42 by Manser et al., 1998. These methods are described in the section Materials and methods.

10 The invention also concerns a vaccine composition as described below, wherein said immunoadjuvant is selected from the group consisting of :

- a polypeptide comprising the amino acid sequence starting at the amino acid residue 720 and ending at the amino acid residue 1014 of sequence SEQ ID N°1,
- 15 - a polypeptide comprising the amino acid sequence starting at the amino acid residue 720 and ending at the amino acid residue 1014 of sequence SEQ ID N°2,
- a polypeptide comprising the amino acid sequence starting at the amino acid residue 720 and ending at the amino acid residue 1014 of sequence SEQ ID N°3,
- 20 - a polypeptide comprising the amino acid sequence starting at the amino acid residue 1146 and ending at the amino acid residue 1451 of sequence SEQ ID N°4,
- a polypeptide comprising the amino acid sequence SEQ ID N°5,
- 25 - a polypeptide comprising the amino acid sequence SEQ ID N°6,
- a polypeptide comprising the amino acid sequence SEQ ID N°7,
- a polypeptide comprising the amino acid sequence SEQ ID N°8, and
- a polypeptide comprising the amino acid sequence SEQ ID N°9.

30 A Rho GTPase activator encompasses peptides comprising the amino acid sequence of interest starting at the amino acid residue 720 and ending at the amino acid residue 1014 of sequence SEQ ID N°1 described above, and comprising a N-terminal amino acid sequence, linked to the amino group of the residue 720 of sequence SEQ ID N°1.

35 Preferably, the N-terminal amino acid sequence has a length up to 800 amino acid residues.

Preferably, the N-terminal amino acid sequence is homologous to a part or to the full length amino acid sequence starting at the amino acid residue 1 and ending at the amino acid residue 719 of CNF1 of SEQ ID N°1.

5 In such a case, the N-terminal amino acid sequence can comprise substitutions of non-essential amino acid comprised in the sequence starting at the amino acid residue 1 and ending at the amino acid residue 719 of CNF1 of SEQ ID N°1.

10 A "non essential" amino acid residue is an amino acid residue that can be altered from the wild type sequence of CNF1 without altering the activating properties of Rho GTPases, whereas an "essential" amino acid residue is required for biological activity.

15 A Rho GTPase activator encompasses also peptides comprising two or more repeated motifs of the sequence 720-1014 of interest. In such a case, said peptide can comprise also an N-Terminal sequence as defined above.

20 A Rho GTPase activator encompasses also peptides structurally similar to those described above, derived from the catalytic domain of CNF2 of sequence SEQ ID N°2, the catalytic domain of CNF<sub>Y</sub> of sequence SEQ ID N°3 and the catalytic domain of DNT of sequence SEQ ID N°4.

25 The use of the catalytic domain of Rho GTPase activator, as described above, is of particular interest. Indeed, as demonstrated in example 3, in the case of CNF1, and DNT, the use of the catalytic domain of these proteins is less toxic for cells than the overall proteins, but is sufficient to confer immunoadjuvanticity.

A Rho GTPase activator encompasses also peptides comprising :

- the amino acid sequence SEQ ID N°5 corresponding to SOPE, or
- the amino acid sequence SEQ ID N°6 corresponding to SOPE2, or
- 30 - The amino acid sequence SEQ ID N°7 corresponding to IpaC, or
- the amino acid sequence SEQ ID N°8 corresponding to CagA, or
- the amino acid sequence SEQ ID N°9 corresponding to the GEF sequence of Dbl,

35 which include more amino acids, and exhibit at least the same activity towards Rho GTPase activation.

Alternatively, the immunoadjuvant according to the invention is selected from the group consisting of :

- a polypeptide comprising the amino acid sequence SEQ ID N°1,
- a polypeptide comprising the amino acid sequence SEQ ID N°2,
- 5 - a polypeptide comprising the amino acid sequence SEQ ID N°3, and
- a polypeptide comprising the amino acid sequence SEQ ID N°4.

Another object of the invention consists in a vaccine composition, wherein said immunoadjuvant compound is a protein comprising a polypeptide consisting of; from the N-terminal end to the C-terminal end, respectively:

- a) the injection domain of a Rho GTPase activator , and
- b) the catalytic domain of a Rho GTPase activator.

By "injection domain of a Rho GTPase activator" it is intended herein, an amino acid sequence allowing the binding and intracellular penetration of a catalytic domain of a Rho GTPase activator.

By "catalytic domain of a Rho GTPase activator" it is intended herein, an amino acid sequence able to activate a Rho GTPase.

The attachment of the injection domain to the catalytic domain above mentioned, to produce a fusion protein may be effected by any means which produces a link between the two constituents, which is sufficiently stable to withstand the conditions used and which does not alter the function of either constituent.

Preferably, the link between them is covalent.

Numerous chemical cross-linking methods are known and potentially applicable for producing the fusion protein. For example, non-specific chemical cross-linking methods, or preferably methods of direct chemical coupling to a functional group, found only once or a few times in one or both of the polypeptides to be cross-linked.

Coupling of the two constituents can also be accomplished via a coupling or conjugating agent. There are several intermolecular cross-linking reagents, which can be used (see, for example, Means, G. E. et al. (1974)). Among these reagents are, for example, N-succinimidyl 3-(2-pyridyldithio) propionate (SPDP) or N, N'-(1,3-phenylene) bismaleimide.



Cross-linking reagents may be homobifunctional, i.e., having two functional groups that undergo the same reaction such as bismaleimido-hexane ("BMH").

Alternatively, to solve the problems of protein denaturation and contamination during chemical conjugation, recombinant techniques can be used to covalently attach the polypeptide of interest to the virulence factor, such as by joining the nucleic acid coding for the polypeptide of interest with the nucleic acid sequence coding for the virulence factor and introducing the resulting gene construct into a cell capable of expressing the conjugate.

Recombinant methodologies required to produce a DNA encoding a desired protein are well known and routinely practiced in the art. Laboratory manuals, for example MOLECULAR CLONING: A LABORATORY MANUAL. Cold Spring Harbor Press: Cold Spring Harbor, N.Y. (1989) describes in detail techniques necessary to carry out the required DNA manipulations.

The fusion protein can be produced in recombinant microorganism transformed therewith. In this process, each protein component is preferably linked in the molecular ratio of 1:1 (injection domain : catalytic domain). The aid of an appropriate linker, in order to allow proper folding of each protein molecule can be useful. As a linker, it is preferable to use a peptide consisting of the appropriate number of amino acids to maintain activity of each protein component, such as, a peptide composed of 0 to 20 amino acids, though glycine, (glycine)<sub>4</sub> serine, or [(glycine)<sub>4</sub> serine]<sub>2</sub>.

Preferable vectors include any of the well known prokaryotic expression vectors, recombinant baculoviruses, COS cell specific vectors, or yeast-specific expression constructs.

Alternatively, the two separate nucleotide sequences can be expressed in a cell or can be synthesized chemically and subsequently joined, using known techniques. Alternatively, the fusion protein can be synthesized chemically as a single amino acid sequence (i.e., one in which both constituents are present) and, thus, joining is not needed.

Preferably, the injection domain of a Rho GTPase activator is a polypeptide selected from the group consisting of :

- a polypeptide comprising the amino acid sequence starting at the amino acid residue 1 and ending at the amino acid residue 719 of sequence SEQ ID N°1;
- 5    - a polypeptide comprising the amino acid sequence starting at the amino acid residue 1 and ending at the amino acid residue 719 of sequence SEQ ID N°2;
- a polypeptide comprising the amino acid sequence starting at the amino acid residue 1 and ending at the amino acid residue 719 of sequence SEQ ID N°3; and
- 10   - a polypeptide comprising the amino acid sequence starting at the amino acid residue 1 and ending at the amino acid residue 1145 of sequence SEQ ID N°4.

Preferably, the catalytic domain of a Rho GTPase activator is a polypeptide selected from the group consisting of :

- 15    - a polypeptide comprising the amino acid sequence starting at the amino acid residue 720 and ending at the amino acid residue 1014 of sequence SEQ ID N°1,
- a polypeptide comprising the amino acid sequence starting at the amino acid residue 720 and ending at the amino acid residue 1014 of sequence SEQ ID N°2,
- 20    - a polypeptide comprising the amino acid sequence starting at the amino acid residue 720 and ending at the amino acid residue 1014 of sequence SEQ ID N°3,
- a polypeptide comprising the amino acid sequence starting at the amino acid residue 1146 and ending at the amino acid residue 1451 of sequence SEQ ID N°4,
- 25    - a polypeptide comprising the amino acid sequence SEQ ID N°5,
- a polypeptide comprising the amino acid sequence SEQ ID N°6,
- a polypeptide comprising the amino acid sequence SEQ ID N°7,
- 30    - a polypeptide comprising the amino acid sequence SEQ ID N°8, and a polypeptide comprising the amino acid sequence SEQ ID N°9.

The invention concerns also the vaccine composition as described above, further comprising an antigen.

- 35    Preferably, the antigen is selected from the group consisting of a hormone, a protein, a drug, an enzyme, a vaccine composition against

bacterial, viral, fungal, prion, or parasitic infections, a component produced by microorganisms, inactivated bacterial toxins such as cholera toxin, ST and LT from *Escherichia coli*, tetanus toxin from *Clostridium tetani*, and proteins derived from HIV viruses.

5       The amount of antigen, and immunoadjuvant compound in the vaccine composition according to the invention, the dosages administered, are determined by techniques well known to those skilled in the pharmaceutical art, taking into consideration such factors as the particular antigen, the age, sex, weight, species, and condition of the  
10       particular animal or patient, and the route of administration.

      In a preferred embodiment, the vaccine composition according to the invention, further comprises one or more components selected from the group consisting of surfactants, absorption promoters, water  
15       absorbing polymers, substances which inhibit enzymatic degradation, alcohols, organic solvents, oils, pH controlling agents, preservatives, osmotic pressure controlling agents, propellants, water and mixture thereof.

      The vaccine composition according to the invention can further comprise a pharmaceutically acceptable carrier. The amount of the  
20       carrier will depend upon the amounts selected for the other ingredients, the desired concentration of the antigen, the selection of the administration route, oral or parenteral, etc. The carrier can be added to the vaccine at any convenient time. In the case of a lyophilised vaccine, the carrier can, for example, be added immediately prior to  
25       administration. Alternatively, the final product can be manufactured with the carrier.

      Examples of appropriate carriers include, but are not limited to, sterile water, saline, buffers, phosphate-buffered saline, buffered sodium chloride, vegetable oils, Minimum Essential Medium (MEM), MEM with  
30       HEPES buffer, etc.

      Optionally, the vaccine composition of the invention may contain conventional, secondary adjuvants in varying amounts depending on the adjuvant and the desired result. The customary amount ranges from about 0.02% to about 20% by weight, depending upon the other  
35       ingredients and desired effect.

Examples of suitable secondary adjuvants include, but are not limited to, stabilizers; emulsifiers; aluminum hydroxide; aluminum phosphate; pH adjusters such as sodium hydroxide, hydrochloric acid, etc.; surfactants such as Tween.RTM. 80 (polysorbate 80, commercially available from Sigma Chemical Co., St. Louis, Mo.); liposomes; iscom adjuvant; synthetic glycopeptides such as muramyl dipeptides; extenders such as dextran or dextran combinations, for example, with aluminum phosphate; carboxypolymethylene; bacterial cell walls such as mycobacterial cell wall extract; their derivatives such as Corynebacterium parvum; Propionibacterium acne; Mycobacterium bovis, for example, Bovine Calmette Guerin (BCG); vaccinia or animal poxvirus proteins; subviral particle adjuvants such as orbivirus; cholera toxin; N,N-diocetadecyl-N',N'-bis(2-hydroxyethyl)-propanediamine (avidine); monophosphoryl lipid A; dimethyldioctadecylammonium bromide (DDA, commercially available from Kodak, Rochester, N.Y.); synthetics and mixtures thereof. Desirably, aluminum hydroxide is admixed with other secondary adjuvants or an immunoadjuvant such as Quil A.

Examples of suitable stabilizers include, but are not limited to, sucrose, gelatin, peptone, digested protein extracts such as NZ-Amine or NZ-Amine AS. Examples of emulsifiers include, but are not limited to, mineral oil, vegetable oil, peanut oil and other standard, metabolizable, nontoxic oils useful for injectables or intranasal vaccines compositions.

For the purpose of this invention, these adjuvants are identified herein as "secondary" merely to contrast with the above-described immunoadjuvant compound, consisting of a Rho GTPase activator, that is an essential ingredient in the vaccine composition for its effect in combination with an antigenic substance to significantly increase the humoral immune response to the antigenic substance. The secondary adjuvants are primarily included in the vaccine formulation as processing aids although certain adjuvants do possess immunologically enhancing properties to some extent and have a dual purpose.

Conventional preservatives can be added to the vaccine composition in effective amounts ranging from about 0.0001% to about 0.1% by weight. Depending on the preservative employed in the formulation, amounts below or above this range may be useful. Typical

preservatives include, for example, potassium sorbate, sodium metabisulfite, phenol, methyl paraben, propyl paraben, thimerosal, etc.

The choice of inactivated, modified or other type of vaccine composition and method of preparation of the improved vaccine composition formulation of the present invention are known or readily  
5 determined by those of ordinary skill in the art.

A pharmacologically effective amount of the immunoadjuvant compound according to the invention may be given, for example orally, parenterally or otherwise, concurrently with, sequentially to or shortly  
10 after the administration of a an antigenic substance in order to potentiate, accelerate or extend the immunogenicity of the antigen.

While the dosage of the vaccine composition depends upon the antigen, species, body weight of the host vaccinated or to be vaccinated, etc., the dosage of a pharmacologically effective amount of the vaccine  
15 composition will usually range from about 50  $\mu$ g to about 500  $\mu$ g per dose, per kilogram of body weight, in a mouse model.

Although the amount of the particular antigenic substance in the combination will influence the amount of the immunoadjuvant compound according to the invention, necessary to improve the immune response, it  
20 is contemplated that the practitioner can easily adjust the effective dosage amount of the immunoadjuvant compound through routine tests to meet the particular circumstances.

As a general rule, the vaccine composition of the present invention is conveniently administered orally, parenterally (subcutaneously, intramuscularly, intravenously, intradermally or intraperitoneally),  
25 intrabuccally, intranasally, or transdermally. The route of administration contemplated by the present invention will depend upon the antigenic substance and the co-formulants. For instance, if the vaccine composition contains saponins, while non-toxic orally or intranasally, care  
30 must be taken not to inject the sapogenin glycosides into the blood stream as they function as strong hemolytics. Also, many antigens will not be effective if taken orally. Preferably, the vaccine composition is administered subcutaneously, intramuscularly or intranasally.

The dosage of the vaccine composition will be dependent upon  
35 the selected antigen, the route of administration, species, body weight

and other standard factors. It is contemplated that a person of ordinary skill in the art can easily and readily titrate the appropriate dosage for an immunogenic response for each antigen to achieve the effective immunizing amount and method of administration.

5       The inventors have also shown, in example 1 that CNF1 has immunoadjuvant properties when coadministered orally with an antigen. They have also shown that this coadministration enhances the total IgA antibody titer in mice. This last result is typical of a mucosal response to an immunisation.

10       Consequently, a further object of the invention is a vaccine composition according to the invention, for administration to a mucosal surface.

      This mode of administration presents a great interest. Indeed, the mucosal membranes contain numerous of dendritic cells and Langerhans cells, which are excellent antigen detecting and antigen presenting cells. The mucosal membranes are also connected to lymphoid organs called mucosal associated lymphoid tissue, which are able to forward an immune response to other mucosal areas. An example of such an epithelia is the nasal epithelial membrane, which consists of practically a single layer of epithelial cells (pseudostratified epithelium) and the mucosal membrane in the upper respiratory tract is connected to the two lymphoid tissues, the adenoids and the tonsils. The extensive network of blood capillaries under the nasal mucosal of the high density of B and T cells, are particularly suited to provide a rapid recognition of the antigen and provide a quick immunological response.

25       Preferably, the mucosal surface is selected from the group consisting of mucosal surfaces of the nose, lungs, mouth, eye, ear, gastrointestinal tract, genital tract, vagina, rectum, and the skin.

      Another object of the invention is a vaccine composition for an oral administration.

30       The invention concerns also a protein comprising a polypeptide consisting of; from the N-terminal end to the C-terminal end, respectively:

- a) the injection domain of a Rho GTPase activator as described above, and

b) the catalytic domain of a Rho GTPase activator as described above.

The invention further concerns the use of a polypeptide of interest, for manufacturing a vaccine composition.

5 The invention also concerns the use of a fusion protein as described above for manufacturing a vaccine composition.

Further details of the invention are illustrated in the following non-limiting examples.

## **MATERIALS AND METHODS**

10

### **Cells and reagents**

Human umbilical vein endothelial cells (HUVEC) were obtained from PromoCell (Heidelberg, Germany). Cells were grown in Human Endothelial SFM medium (Invitrogen Co, Paisley, Scotland) supplemented with defined growth factors (d-SFM): 10 ng/ml EGF and 20  
15 ng/ml bFGF (Invitrogen Co), 1 µg/ml heparin (Sigma-Aldrich) and either 20% foetal bovine serum (Invitrogen Co) or 1% (W/V) bovine serum albumin (ELISA grade, Sigma-Aldrich) together with penicillin and streptomycin (Invitrogen Co). Cells were grown on 0,2% gelatine coated  
20 dishes (Sigma-Aldrich). Transfections of HUVEC were carried out as described by Mettouchi et al., 2001. Antibodies used were monoclonal anti-β actin antibody [clone AC-74] (Sigma-Aldrich); anti-RhoA, anti-Cdc42, anti-Rac1 and anti-Ras antibodies (Transduction Laboratories); anti-HA [clone 11] (BabCO); anti-E-selectin [clone CTB202] (Santa Cruz  
25 Biotechnology) and rabbit polyclonal anti-phospho-p44/42 MAP kinase (Thr202/Tyr204), anti phospho-p38 MAP kinase (Thr180/Tyr182) and anti phospho-c-Jun (Ser73) (Cell Signaling Technology); anti-human IκB-α (Upstate Biotechnology); anti-TRAF1 (H-186, Santa Cruz Biotechnology). Primary antibodies were visualized using goat anti-  
30 mouse or anti-rabbit horseradish peroxidase-conjugated secondary antibodies (DAKO, Glostrup, Denmark). TRAF1 rabbit antibodies were visualized using biotin-XX goat anti-rabbit IgG followed by streptavidin horseradish peroxidase conjugate (Molecular Probes). DNA vectors corresponding to pcDNA3RhoQ63L, RacQ61L and Cdc42Q61L were  
35 provided by Manor, D. ( Lin et al., 1999).

### **Immunizations and immune response measurements.**

Female BALB/c mice were purchased from Charles River Laboratories (L'Arbresle, France). Animals were maintained and handled according to the regulations of the European Union and French Department of Health. In all experiments 4-8 week-old female mice were immunized. Mice were fed with either CNF1 or CNF1-C866S or CT in the presence of 5 mg ovalbumin (OVA) (grade V, Sigma-Aldrich) dissolved in a solution of 500µl of 3% NaHCO<sub>3</sub>. Levels of anti-OVA antibodies were determined by means of solid-phase ELISA, as previously described by Anjuère et al., 2003. Mucosal anti-OVA IgA titers were determined according to the PERFEXT method (Villavedra et al., 1997). Briefly, guts were collected, weighted and homogenized 1:1 (W/V) in PBS supplemented with 2% saponin (SIGMA) and protease inhibitors (complete, Boehringer). IgA titers were determined by means of solid-phase ELISA, as previously described (Anjuère et al., 2003). Antibodies used were goat anti-mouse IgG, IgG1, IgG2a, IgG2b and IgA, horseradish peroxidase conjugated (SouthernBiotech, Birmingham, USA).

### **DNA array analysis**

HUVEC were seeded at  $8 \times 10^6$  cells/150 mm gelatin-coated dish in d-SFM containing BSA. Cells were intoxicated in parallel for 3h and 24h in d-SFM/BSA supplemented with  $10^{-9}$ M CNF1. Cells were lysed in RTL buffer for total RNA extraction, according to the manufacturer (RNeasy MiniKit, Qiagen). CNF1 regulated genes were analyzed using Affymetrix® Human GeneChip U133A and U133B, by Aros Applied Biotechnology ApS ([www.arosab.com](http://www.arosab.com)), as recommended by the manufacturer ([www.Affymetrix.com](http://www.Affymetrix.com)).

### **Toxins**

Purified cholera toxin (CT) was obtained from List Biologicals (Campbell, CA). For CNF1 and CNF1-C866S toxin purification, *E. coli* OneShot, carrying pCR2cnf1 or pCR2cnf1C866S were grown overnight at 37°C in LB medium. Bacteria were harvested by centrifugation, suspended in 30 ml PBS and lysed using a French Press. The lysate was centrifuged 30



000 x g for 30 min, at 4°C and the supernatant was precipitated with the same volume of saturated ammonium sulphate for 5-8 hours. Precipitate was then dialysed against TN buffer ( 25 mM Tris [pH 7.4], 50 mM NaCl) and applied on a DEAE fast flow column (11 x 1.5 cm ; Pharmacia Biotech, Uppsala, Sweden). The column was washed for 200 min with the same buffer (1ml/min). CNF1 was eluted with a 50 to 300 mM NaCl gradient during 100 min (elution around 200 mM NaCl). The fractions containing CNF1 were pooled, dialysed against TN buffer and applied on a Superdex 75 column (0.3 ml/min ; Pharmacia Biotech). The fractions containing CNF1 were pooled, concentrated and applied on a monoQ column (Pharmacia Biotech). After a 20 min wash (1ml/min) of the column with TN buffer, CNF1 was eluted using a 50 to 400 mM NaCl gradient (elution around 350 mM NaCl). CNF1 purification was followed by SDS-PAGE. The activity of the different batches of CNF1 toxin was estimated by HEp-2 cells multinucleation assay, as previously described (Lemichez et al., 1997). The purified CNF1 toxin used in this study produced at  $10^{-12}$  M 50% of multinucleation of HEp-2 cells after 48 hours of intoxication.

## 20 **ELISA**

HUVEC were seeded 24h before toxin addition at  $2 \times 10^5$  cells/ 22.5 mm or  $5 \times 10^5$  cells/ 35 mm well in d-SFM containing serum. Intoxication of cells was performed by addition of fresh medium containing CNF1, for different periods of time. One hour before intoxication ending the medium was replaced by d-SFM containing BSA for ELISA. IL-8, MCP-1, IL-6, MIP3- $\alpha$ , TNF- $\alpha$  and RANTES production were assessed using human Quantikine<sup>®</sup> immunoassays, as recommended by the manufacturer (R & D Systems, Abingdon, UK).

## 30 **Pull-down and immunoblotting detection of activated-Rho GTPases**

Levels of activated-RhoA, -RhoB, -RhoC, -Rac1, -Rac2, -Cdc42 were measured using classical Rho effector pull-down assays developed by Manser et al., 1998 and Ren et al., 1999. For antibodies description see the cells and reagents section.

Briefly, the measure of the levels of activated-RhoA, -B and -C was performed as followed. Cells were lysed in 50mM Tris, pH7.2, 500mM NaCl, 10mM MgCl<sub>2</sub>, 1% Triton X-100, 0.5% deoxicholate, 0.1% SDS and protease inhibitors. Cell lysates were clarified by centrifugation at 13000g at 4°C for 10min. and equal volumes of lysates (corresponding to 1mg of total proteins) were incubated with 30 micrograms GST-RBD (Rho binding domain of Rhotekin fused to GST and described in Ren et al., 1999) beads at 4°C for 45min. The beads were washed four times with buffer B (50mM Tris, pH7.2, 500mM NaCl, 10mM MgCl<sub>2</sub>, 1% Triton X-100 and protease inhibitors). Bound Rho proteins were resolved by SDS-PAGE and transferred on PVDF membranes. Activated-Rho proteins were detected by immunoblotting using a monoclonal antibody against either RhoA and RhoC or RhoB and anti-mouse horseradish peroxidase-conjugated secondary antibody followed by chemiluminescence detection.

The measure of the levels of activated-Rac1, Rac2 and Cdc42 was determined, as followed. Cells were lysed in LB buffer (25 mM Tris, pH7.5, 150mM NaCl, 5mM MgCl<sub>2</sub>, 0.5% Triton X-100, 4% glycerol and protease inhibitors). Cell lysates were clarified by centrifugation at 13000g at 4°C for 10min. and equal volumes of lysates (corresponding to 1mg of total proteins) were incubated with 30 micrograms GST-PAK70-106 (Rac/Cdc42 binding domain of p21PAK fused to GST and described in Manser et al., 1998) beads at 4°C for 45min. The beads were washed four times with LB. Bound Rac and Cdc42 proteins were resolved by SDS-PAGE and transferred on PVDF membranes. Activated-Rac1, 2 or activated-Cdc42 proteins were detected by immunoblotting using a monoclonal antibody against either Rac1, 2 or Cdc42 and anti-mouse horseradish peroxidase-conjugated secondary antibody followed by chemiluminescence detection.

For activated Ras measurements GST-RBD1-149 of Raf1 was used as described by the authors (de Rooij and Bos, 1997).

### **Example 1: CNF1 effects on cell signaling pathways**

Kinetics of CNF1-induced Rac1, Cdc42 and RhoA activation have been

studied. These kinetics show the specificity of Rho protein activation, as compared to the Ras GTPase (Fig. 1A, 1B). Obviously, these measurements do not represent an exhaustive list of the Rho proteins activated by CNF1, other Rho bearing the canonical sequence for CNF1 recognition/modification (Lerm et al., 1999). These measurements rather indicated that all the three Rho proteins exhibited a maximal activation around 2 hours in HUVEC intoxicated with  $10^{-9}$ M CNF1 (Fig. 1B). CNF1 interference with classical signaling pathways leading to gene regulation, has also been shown. Consistent with the absence of Ras activation measured, CNF1 did not produce ERK1/2 phosphorylation (Fig. 1A, 1C). CNF1 rather appeared to interfere both with the SAP-kinase signaling pathways, unraveled by p38MAP-kinase and cjun phosphorylations. CNF1 also interferes with the NF-kappaB pathway, as shown by I $\kappa$ B depletion (Fig. 1C). Host cells have evolved cell surface receptors to get alarmed of the presence of PAMP (Medzhitov and Janeway, 2002). PAMP receptors initiate an innate immune response through I $\kappa$ B depletion for NF $\kappa$ B activation (Barton and Medzhitov, 2003). That cell treatment with the catalytic inactive CNF1-C866S toxin was devoid of interference with all signaling pathways tested, especially NF $\kappa$ B, strongly suggested an absence of cell recognition of CNF1 as a PAMP (Fig. 1C).

#### **Example 2 : CNF1 potentiates host adaptative responses to a bystander antigen.**

The systemic and mucosal humoral immune responses in mice fed CNF1 together with ovalbumin (OVA), a prototype soluble protein antigen, has been studied. Oral co-administration of OVA and CNF1 induced serum IgG antibody responses to OVA that were almost comparable in magnitude to those evoked by cholera toxin (CT) (Fig. 2A), the most potent mucosal adjuvant (Holmgren et al., 2003). These responses were comprised predominantly of IgG1 and IgG2b, indicating a bias toward a classical Th-2 response (Fig 2B). Feeding OVA alone failed to induce detectable antibody responses (not shown). Furthermore, feeding mice CNF1 evoked strong IgA antibody responses to co-administered OVA in the small intestinal mucosal (Fig. 2C). Taken

together, these results demonstrate that CNF1 displays adjuvant properties on gut-induced mucosal and systemic immune responses. To examine whether CNF1 catalytic activity was required to support the adjuvanticity of this toxin, the effects of wild type CNF1 to that of the enzymatically inactive mutant (CNF1-C866S) have been compared. The results show that the enzymatic activity of CNF1 is necessary to promote its adjuvanticity for systemic as well as mucosal anti-OVA antibody responses (Fig. 2). In conclusion, this study indicates that CNF1-induced activation of Rho proteins efficiently triggers a host cell alarm program and suggests that this toxin is endowed immunomodulatory properties on innate and adaptative immune responses.

**Example 3 The catalytic domain of DNT remains active on cells and is sufficient to confer adjuvanticity**

CNF1 belongs to a family of toxins among them DNT, having similar catalytic activity (Boquet and Lemichez 2003). It is shown on Figure 3A that the catalytic domain of DNT (DNT-CTER) remains active on cells, although showing a lower intoxication property as compared to CNF1. Despite its inability to intoxicate cells (Fig. 3A), the catalytic domain of CNF1 (CNF1-CTER) upon mechanical injection into cells produces a *bona fide* toxic phenotype (Lemichez et al., 1997). It has been taken advantage of the above observations to test the adjuvant properties of the catalytic domains of both toxins. Mice were fed 10 times higher quantities of both toxin catalytic domains, as compared to CNF1. In these conditions it has been observed that DNT-CTER stimulated significantly the anti-OVA IgG responses (Fig. 3B). CNF1-CTER also produced a stimulation of the anti-OVA IgG responses, although at a lower level (Fig. 3B). Taken together, these results indicate that the adjuvanticity of this group of toxin is encompassed in their catalytic domain. Nevertheless, the injection domain of CNF1-toxin together with its catalytic domain, allows the use of lower doses to induce a significantly higher biological effect.

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### Claims

1. A vaccine composition comprising an immunoadjuvant compound,  
wherein said immunoadjuvant compound consists of a Rho GTPase  
activator.
2. A vaccine composition according to claim 1 wherein said  
immunoadjuvant compound is selected from the group consisting of :
  - a polypeptide comprising the amino acid sequence starting at the  
amino acid residue 720 and ending at the amino acid residue 1014 of  
sequence SEQ ID N°1,
  - a polypeptide comprising the amino acid sequence starting at the  
amino acid residue 720 and ending at the amino acid residue 1014 of  
sequence SEQ ID N°2,
  - a polypeptide comprising the amino acid sequence starting at the  
amino acid residue 720 and ending at the amino acid residue 1014 of  
sequence SEQ ID N°3,
  - a polypeptide comprising the amino acid sequence starting at the  
amino acid residue 1146 and ending at the amino acid residue 1451  
of sequence SEQ ID N°4,
  - a polypeptide comprising the amino acid sequence SEQ ID N°5,
  - a polypeptide comprising the amino acid sequence SEQ ID N°6,
  - a polypeptide comprising the amino acid sequence SEQ ID N°7,
  - a polypeptide comprising the amino acid sequence SEQ ID N°8, and
  - a polypeptide comprising the amino acid sequence SEQ ID N°9.
3. A vaccine composition according to claim 1 wherein said  
immunoadjuvant compound is selected from the group consisting of :
  - a polypeptide comprising the amino acid sequence SEQ ID N°1,
  - a polypeptide comprising the amino acid sequence SEQ ID N°2,
  - a polypeptide comprising the amino acid sequence SEQ ID N°3, and
  - a polypeptide comprising the amino acid sequence SEQ ID N°4.

4. A vaccine composition according to claim 1, wherein said immunoadjuvant compound is a protein comprising a polypeptide consisting of; from the N-terminal end to the C-terminal end, respectively:
- 5 a) the injection domain of a Rho GTPase activator , and  
b) the catalytic domain of a Rho GTPase activator.
5. A vaccine composition according to claim 4, wherein said injection domain of a Rho GTPase activator is a polypeptide selected from the group consisting of :
- 10 - a polypeptide comprising the amino acid sequence starting at the amino acid residue 1 and ending at the amino acid residue 719 of sequence SEQ ID N°1;  
- a polypeptide comprising the amino acid sequence starting at the amino acid residue 1 and ending at the amino acid residue 719 of sequence SEQ ID N°2;
- 15 - a polypeptide comprising the amino acid sequence starting at the amino acid residue 1 and ending at the amino acid residue 719 of sequence SEQ ID N°3; and  
- a polypeptide comprising the amino acid sequence starting at the amino acid residue 1 and ending at the amino acid residue 1145 of sequence SEQ ID N°4.
- 20
6. A vaccine composition according to anyone of claims 4 and 5, wherein said catalytic domain of a Rho GTPase activator is a polypeptide selected from the group consisting of :
- 25 - a polypeptide comprising the amino acid sequence starting at the amino acid residue 720 and ending at the amino acid residue 1014 of sequence SEQ ID N°1,  
- a polypeptide comprising the amino acid sequence starting at the amino acid residue 720 and ending at the amino acid residue 1014 of sequence SEQ ID N°2,
- 30 - a polypeptide comprising the amino acid sequence starting at the amino acid residue 720 and ending at the amino acid residue 1014 of sequence SEQ ID N°3,
- 35

- a polypeptide comprising the amino acid sequence starting at the amino acid residue 1146 and ending at the amino acid residue 1451 of sequence SEQ ID N°4,
  - a polypeptide comprising the amino acid sequence SEQ ID N°5,
  - 5 - a polypeptide comprising the amino acid sequence SEQ ID N°6,
  - a polypeptide comprising the amino acid sequence SEQ ID N°7,
  - a polypeptide comprising the amino acid sequence SEQ ID N°8, and
  - a polypeptide comprising the amino acid sequence SEQ ID N°9.
- 10 7. A vaccine composition according to anyone of claim 1-6 comprising further an antigen.
8. A vaccine composition according to claim 7 wherein the antigen is selected from the group consisting of a hormone, a protein, a drug, an  
15 enzyme, a vaccine composition against bacterial, viral, fungal, prion, or parasitic infections, a component produced by microorganisms, inactivated bacterial toxins such as cholera toxin, ST and LT from *Escherichia coli*, tetanus toxin from *Clostridium tetani*, and proteins derived from HIV viruses.
- 20 9. A vaccine composition according to anyone of claims 1-8 for administration to a mucosal surface.
10. A vaccine composition according to anyone of claims 1-9, for an oral  
25 administration.
11. A protein comprising a polypeptide consisting of; from the N-terminal end to the C-terminal end, respectively :  
a) the injection domain of a Rho GTPase activator according to  
30 anyone of claims 4 and 5, and  
b) the catalytic domain of a Rho GTPase activator according to anyone of claims 4 and 6.
12. Use of a polypeptide as defined in anyone of claim 1-6 for  
35 manufacturing a vaccine composition.

13. Use of a protein according to claim 11 for manufacturing a vaccine composition.

ABSTRACT OF DISCLOSURE

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A vaccine composition comprising an Immunoadjuvant compound consisting of a Rho GTPase family activator

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INSTITUT NATIONAL DE LA SANTE ET DE LA  
RECHERCHE MEDICALE INSERM

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This invention is based on the experimental finding that activators of Rho GTPases, namely the cytotoxic necrotizing factor 1 (CNF1), and DNT bear immunostimulatory properties towards the systemic response to orally administered ovalbumine.

This invention concerns a vaccine composition comprising an immunoadjuvant compound, wherein said immunoadjuvant compound consists of a Rho GTPase activator.





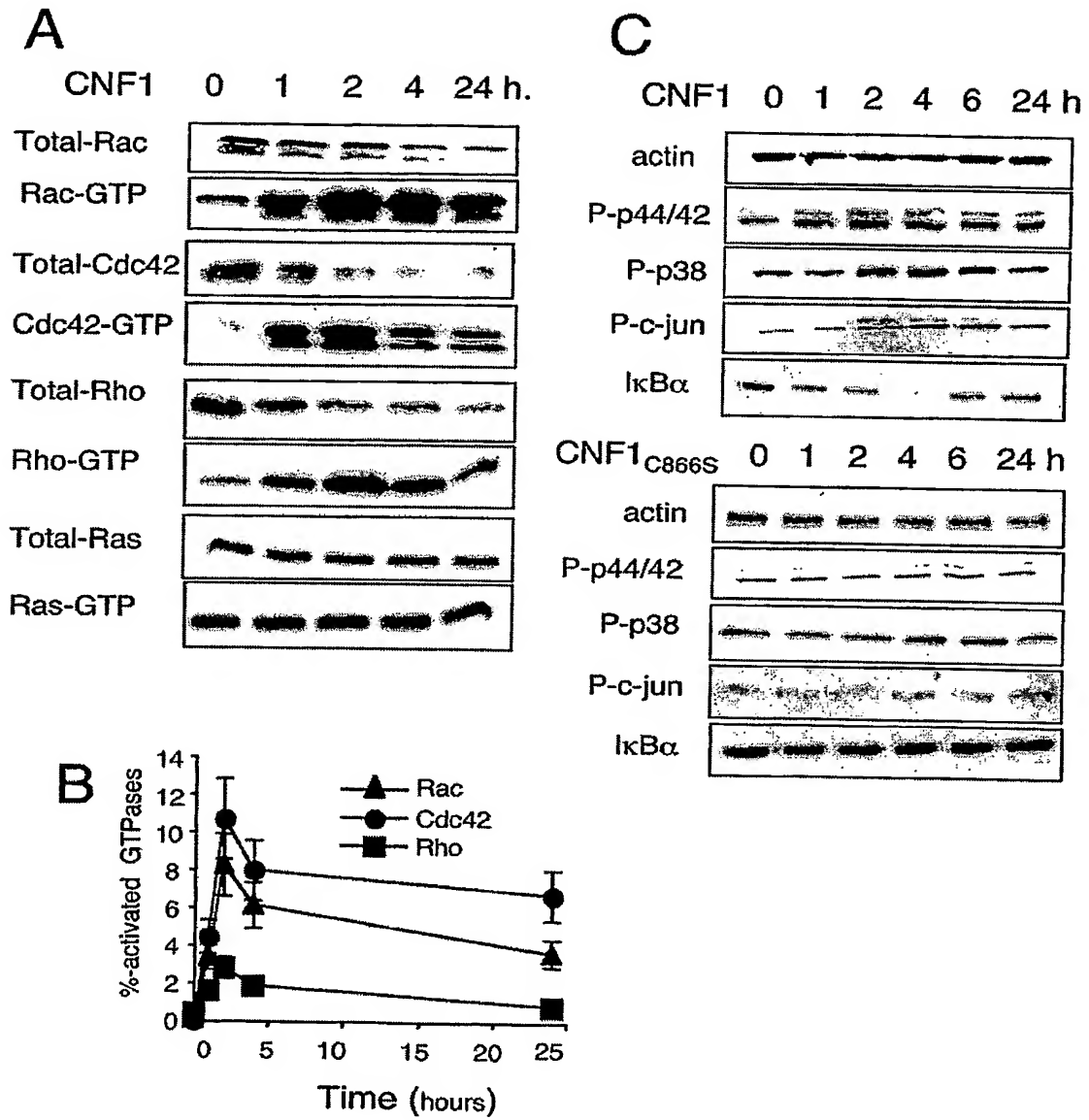


FIGURE 1

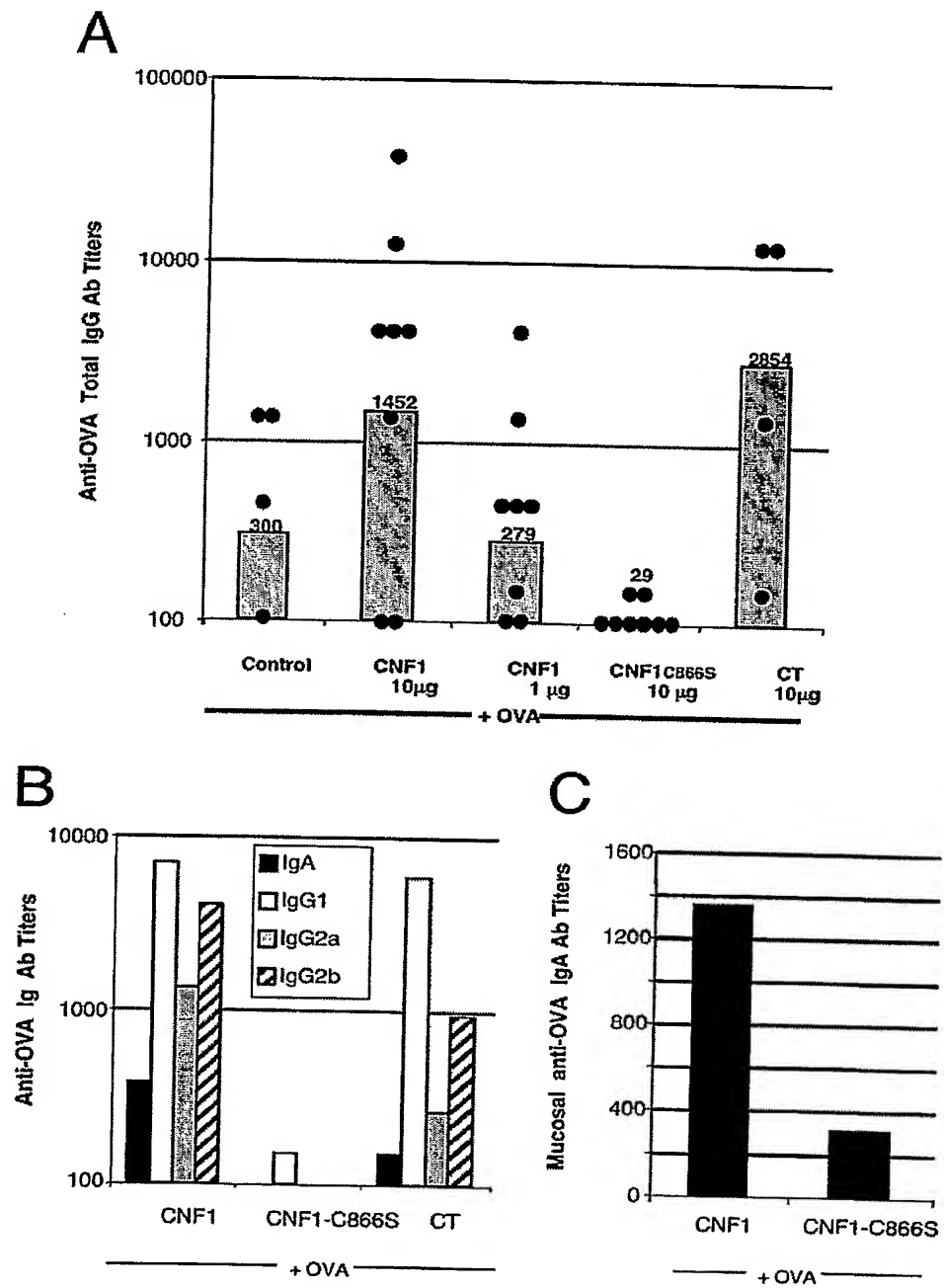
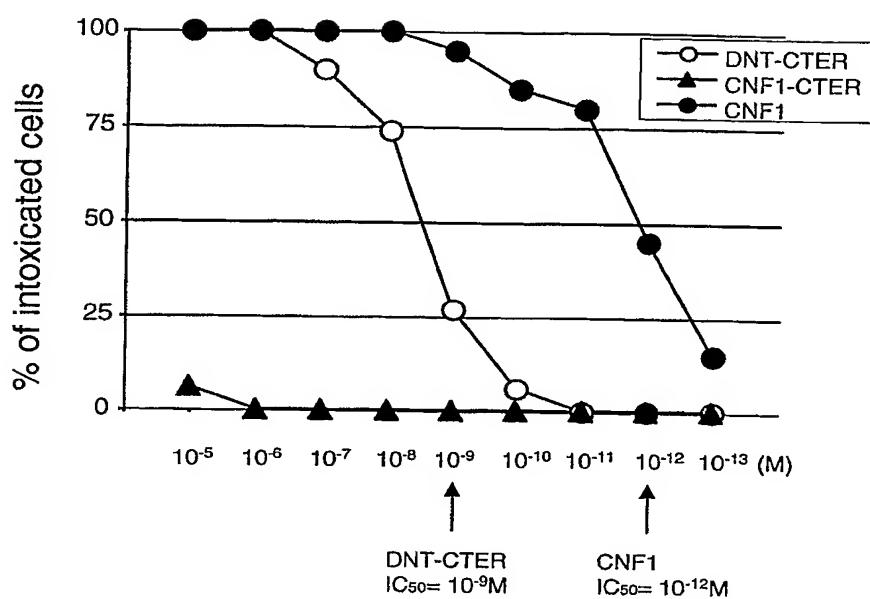


FIGURE 2

3/3

A



B

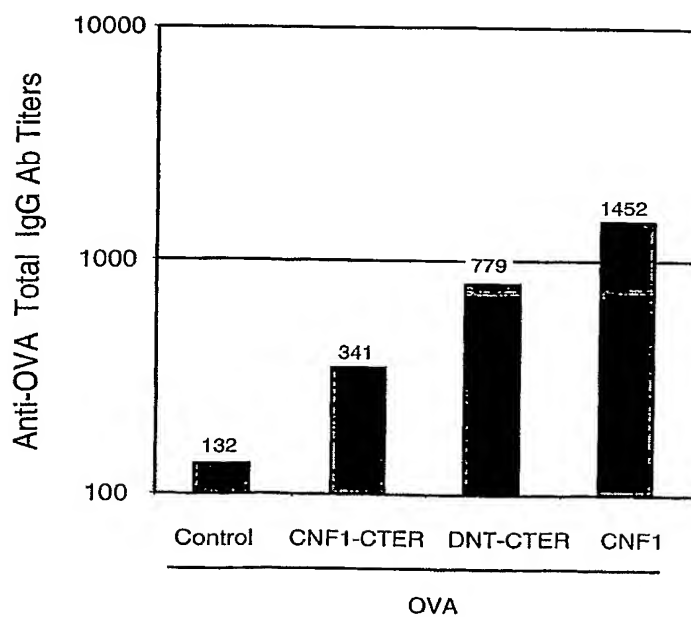


FIGURE 3



# SEQUENCE LISTING

<110> INSERM

<120> A vaccine composition comprising an immunoadjuvant compound consisting of a Rho GTPase family activator

<130> Q971EP

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<170> PatentIn version 3.1

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Asn Ala Tyr Phe Ile Cys Phe Ser Gln Asn Arg Ser Asn Ser Arg Ser  
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Tyr Thr Gly Trp Asp His Leu Gly Lys Tyr Lys Thr Glu Val Leu Thr  
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Leu Thr Gln Ala Ala Leu Ile Asn Ile Gly Tyr Arg Phe Asp Val Phe  
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Asp Asp Ala Asn Ser Ser Thr Gly Ile Tyr Lys Thr Lys Ser Ala Asp  
100 105 110

Val Phe Asn Glu Glu Asn Glu Glu Lys Met Leu Pro Ser Glu Tyr Leu  
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His Phe Leu Gln Lys Cys Asp Phe Ala Gly Val Tyr Gly Lys Thr Leu  
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Ser Asp Tyr Trp Ser Lys Tyr Tyr Asp Lys Phe Lys Leu Leu Leu Lys  
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Thr	Leu	Lys	Glu	Leu	Ile	Lys	Asp	Ser	Asp	Lys	Gln	Gln	Leu	Leu	Ser				
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Asp	Ala	Ile	Ala	Ile	Ser	Val	Lys	Lys	Arg	Ser	Phe	Ser	Asp	Gly	Asp				
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Ser	Phe	Ala	Ile	Pro	Leu	Leu	Ile	Ser	Lys	Ala	Gly	Ile	Asn	Gln	Glu				
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Lys Gly Ser Ser Leu Ser Gly Ile Tyr Tyr Glu Val Asp Ile Glu Thr  
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Glu Ile Leu Trp Thr Arg Gly Gly Gly Leu Lys Gly Gly Gln Pro Phe  
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785 790 795 800

Thr Tyr Trp Lys Lys Tyr Asn Leu Thr Asn Glu Thr Ser Ile Ile Arg  
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Glu Val Gln Glu Gly Lys Pro Val Ile Ile Thr Ser Gly Asn Leu Ser  
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His Thr Gly Thr Thr Lys Ser Leu Ala Gly Phe Thr Ser Thr Thr Gly  
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Val Lys Lys Ala Val Glu Val Leu Glu Leu Leu Thr Lys Glu Pro Ile  
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Pro Arg Val Glu Gly Ile Met Ser Asn Asp Phe Leu Val Asp Tyr Leu  
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Ser Glu Asn Phe Glu Asp Ser Leu Ile Thr Tyr Ser Ser Ser Glu Lys  
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Tyr Thr Gly Trp Asp His Leu Gly Lys Tyr Lys Thr Gly Val Leu Thr  
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Asp Asp Ala Asn Ala Ser Ala Gly Ile Tyr Lys Thr Ser Ser Ala Asp  
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Gln His Phe Ser Leu Tyr Ser Arg Gln Asp Gly Ile Thr Tyr Ala Gly  
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Ala Ile Tyr Pro Tyr Phe Glu Ser Ala Asn Ala Asp Glu Gln Gln Pro  
755 760 765

Val Phe Phe Tyr Ile Lys Lys Asn Arg Phe Asp Asp Phe Gly Tyr Asp  
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Gln Tyr Phe Tyr Asn Ser Thr Val Gly Leu Asn Gly Ile Pro Thr Leu  
785 790 795 800

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835	840	845
Glu Val Gln Glu Gly Lys Pro Val Ile Ile Thr Ser Gly Asn Leu Ser		
850	855	860
Gly Cys Thr Thr Ile Val Ala Arg Lys Gly Gly Tyr Leu Tyr Lys Val		
865	870	875
His Thr Gly Thr Thr Ile Pro Leu Ala Gly Phe Thr Ser Thr Thr Gly		
	885	890
Val Lys Lys Ala Val Glu Val Phe Glu Leu Leu Thr Asn Asn Pro Met		
	900	905
Pro Arg Val Glu Gly Val Met Asn Asn Asp Phe Leu Val Asn Tyr Leu		
	915	920
Ala Glu Ser Phe Asp Glu Ser Leu Ile Thr Tyr Ser Ser Ser Glu Gln		
	930	935
Lys Ile Gly Ser Lys Ile Thr Ile Ser Arg Asp Asn Val Ser Thr Phe		
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Pro Tyr Phe Leu Asp Asn Ile Pro Glu Lys Gly Phe Gly Thr Ser Val		
	965	970
Thr Ile Leu Val Arg Val Asp Gly Asn Val Ile Val Lys Ser Leu Ser		
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His Lys Phe Ser Thr Thr Leu Pro Trp Phe Gly Trp Ala Asp Pro Asp  
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Asn Leu Tyr Phe Ile Arg Phe Thr Gln Ser Arg Ser Asn Asn Lys Ser  
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Tyr Thr Gly Trp Asp His Leu Gly Lys Tyr Ala Ile Glu Thr Leu Thr  
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Leu Thr Gln Ala Ala Ile Val Asn Ile Gly Ser Arg Phe Asp Ile Phe  
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Asp Glu Ala Asn Ser Thr Ala Gly Ile Tyr Lys Thr Asn Asn Ala Asp  
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Ser Phe Asp Glu Thr Asn Glu Ala Lys Met Leu Pro Ser Glu Tyr Leu  
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Tyr Phe Leu Arg Asp Cys Asp Phe Ser Asn Leu Tyr Asn Lys Ala Leu  
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Ser Asp Tyr Trp Ala Glu Asn Tyr Glu Lys Phe Ser Thr Leu Leu Gln  
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Asn Tyr Tyr Ile Ser Ser Ala Tyr Tyr Leu Tyr Lys Asp Ser Ala Ile  
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Ser Lys Asp Glu Tyr Glu Phe Ser Ile Asp Ala Ile Phe Asn Lys Lys  
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Ser Lys Ile Leu Arg Tyr Tyr Phe Asp Val Tyr Gly Tyr Tyr Ser Ser  
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Asp Met Phe Val Ala Met Asn Asp Asn Lys Thr Met Leu Phe Ile Pro  
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Gly Ala Thr Asn Pro Phe Ile Phe Ala Asp Asn Ile Thr Asp Leu Arg  
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Asp Lys Ile Lys Ala Leu Ile Ser Asp Lys Asn Thr Arg Glu Leu Phe  
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Ser Lys His Phe Ser Leu Tyr Asp Arg Gln Asp Gly Asn Thr Tyr Leu  
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Gly Val Asn Ser Met Leu Glu Gln Ile Val Ser Gly Val Val Asp Thr  
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Asn Tyr Ile Met Tyr Ser Asn Lys Asn Ile Arg Glu Arg Asn Val Phe  
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Gly Ser Met Ala Phe Ser Thr Arg Glu Arg Ser Phe Asn Asp Gly Asp  
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Val Ile Ile Lys Ser Asn Ala Glu Val Gln Arg Asp Tyr Ala Leu Asn  
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Pro Glu Val Ser Ile Pro Ile Ser Leu Gly Ile Thr Ala Ser Ser Val  
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Gly Ile Ser Phe Asp Glu Leu Ile Asn Gly Asp Thr Tyr Glu Glu Arg  
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Arg Ser Ala Ile Pro Gly Leu Ala Thr Asn Thr Val Leu Leu Gly Ile  
385 390 395 400

Ser Phe Ala Ile Pro Phe Leu Ile Ser Lys Ala Glu Glu Asn Lys Leu  
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Ile Ile Asn Asn Leu Val Gly Ser Asp Glu Asn Ile Leu Asn Lys Asn  
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Asn Leu Gly Asp Phe Leu Glu Lys Tyr Asn Ile Ser Glu Ser Asp Ile  
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Pro Glu Asn Gly Ser Leu Val Ile Asn Leu Lys Asn Thr Asn Val Pro  
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Val Arg Leu Val Lys Leu Asn Asp Glu Glu Gly Glu Ile Val Ala Ile  
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485 490 495

Gly Tyr Glu Ile Leu Ser Arg Arg Val Phe Arg Thr Glu Tyr Asn Glu



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Pro	Leu	Leu	Phe	Pro	Glu	Met	Asp	Ser	Arg	Leu	Pro	Lys	Pro	Thr	Pro
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Glu	Leu	Asp	Ile	Lys	Tyr	Tyr	Ser	Ser	Asn	Leu	Ser	Ser	Phe	Lys	Glu
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Asp	Thr	Val	Ile	Leu	Met	Arg	Gly	Thr	Thr	Glu	Glu	Glu	Ala	Trp	Asn
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Val	Ala	Glu	Ile	Ser	Ser	Ile	Asn	Phe	Arg	Arg	Leu	Asn	Ser	Gly	Asn
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785 790 795 800

Asn Thr Tyr Thr Gly Glu Tyr Val Ala Asp Ser Ser Ser Gln Gly Ala  
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Thr Tyr Trp Leu Lys Tyr Asn Leu Thr Asn Glu Thr Ser Ile Ile Lys  
820 825 830

Val Ser Asn Ser Ala Arg Gly Ala Asn Gly Ile Lys Ile Ala Leu Glu  
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Glu Ile Glu Glu Asn Lys Pro Val Val Ile Thr Ser Gly Thr Leu Thr  
850 855 860

Gly Cys Thr Val Val Phe Ala Arg Lys Gly Glu Tyr Phe Tyr Ala Val  
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His Thr Gly Asn Ser Glu Ser Leu Ile Gly Phe Thr Ser Thr Ser Gly  
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Pro Ala Leu Pro Asp Val Ile Asn Asn Asn Thr Leu Val Glu Tyr Leu  
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180

185

190

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Glu Met Pro Arg Lys Leu Asp Ala Trp Glu Ile Ala Lys Phe His Leu  
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Val Ser Met Ala Ala Ala Leu Ile Ala Gly Val Leu Cys Asp Leu Glu  
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420 425 430

Asp	Phe	Arg	Asp	Ser	Asp	Ala	Phe	Ala	Ser	Tyr	Ala	Glu	Tyr	Ala	Ala	435	440	445	
Gln	Phe	Asn	Asp	Tyr	Ile	Asp	Gln	Tyr	Ser	Ile	Leu	Glu	Ala	Gln	Arg	450	455	460	
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Cys	Leu	Pro	Leu	Gln	Lys	Val	Arg	His	Tyr	Lys	Val	Leu	Thr	Ser	Gln	485	490	495	
Pro	Gly	Leu	Ile	Ala	Arg	Gly	Ile	Glu	Asn	His	Asn	Arg	Gly	Ile	Glu	500	505	510	
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Met	Phe	Gln	Leu	His	Asp	Ser	Ser	Trp	Leu	Leu	Val	Ser	Asn	Ile	Asn	530	535	540	
Gly	Glu	Leu	Trp	Ser	Asp	Val	Leu	Ala	Asn	Ala	Glu	Val	Met	Gln	Asn	545	550	555	560
Pro	Thr	Leu	Ala	Ala	Leu	Ala	Glu	Pro	Gln	Gly	Arg	Phe	Arg	Thr	Gly	565	570	575	
Arg	Arg	Thr	Gly	Gly	Trp	Phe	Leu	Gly	Gly	Pro	Ala	Thr	Glu	Gly	Pro	580	585	590	
Ser	Leu	Arg	Asp	Asn	Tyr	Leu	Leu	Lys	Leu	Arg	Gln	Ser	Asn	Pro	Gly	595	600	605	
Leu	Asp	Val	Lys	Lys	Cys	Trp	Tyr	Phe	Gly	Tyr	Arg	Gln	Glu	Tyr	Arg	610	615	620	
Leu	Pro	Ala	Gly	Ala	Leu	Gly	Val	Pro	Leu	Phe	Ala	Val	Ser	Val	Ala	625	630	635	640
Leu	Arg	His	Ser	Leu	Asp	Asp	Leu	Ala	Ala	His	Ala	Lys	Ser	Ala	Leu	645	650	655	
Tyr	Lys	Pro	Ser	Glu	Trp	Gln	Lys	Phe	Ala	Phe	Trp	Ile	Val	Pro	Phe	660	665	670	

Tyr Arg Glu Ile Phe Phe Ser Thr Gln Asp Arg Ser Tyr Arg Val Asp  
675 680 685

Val Gly Ser Ile Val Phe Asp Ser Ile Ser Leu Leu Ala Ser Val Phe  
690 695 700

Ser Ile Gly Gly Lys Leu Gly Ser Phe Thr Arg Thr Gln Tyr Gly Asn  
705 710 715 720

Leu Arg Asn Phe Val Val Arg Gln Arg Ile Ala Gly Leu Ser Gly Gln  
725 730 735

Arg Leu Trp Arg Ser Val Leu Lys Glu Leu Pro Ala Leu Ile Gly Ala  
740 745 750

Ser Gly Leu Arg Leu Ser Arg Ser Leu Leu Val Asp Leu Tyr Glu Ile  
755 760 765

Phe Glu Pro Val Pro Ile Arg Arg Leu Val Ala Gly Phe Val Ser Ala  
770 775 780

Thr Thr Val Gly Gly Arg Asn Gln Ala Phe Leu Arg Gln Ala Phe Ser  
785 790 795 800

Ala Ala Ser Ser Ser Ala Gly Arg Thr Gly Gly Gln Leu Ala Ser Glu  
805 810 815

Trp Arg Met Ala Gly Val Asp Ala Thr Gly Leu Val Glu Ser Thr Ser  
820 825 830

Gly Gly Arg Phe Glu Gly Ile Tyr Thr Arg Gly Leu Gly Pro Leu Ser  
835 840 845

Glu Cys Thr Glu His Phe Ile Val Glu Ser Gly Asn Ala Tyr Arg Val  
850 855 860

Ile Trp Asp Ala Tyr Thr His Gly Trp Arg Val Val Asn Gly Arg Leu  
865 870 875 880

Pro Pro Arg Leu Thr Tyr Thr Val Pro Val Arg Leu Asn Gly Gln Gly  
885 890 895

His Trp Glu Thr His Leu Asp Val Pro Gly Arg Gly Gly Ala Pro Glu  
900 905 910

Ile Phe Gly Arg Ile Arg Thr Arg Asn Leu Val Ala Leu Ala Ala Glu  
915 920 925

Gln Ala Ala Pro Met Arg Arg Leu Leu Asn Gln Ala Arg Arg Val Ala  
930 935 940

Leu Arg His Ile Asp Thr Cys Arg Ser Arg Leu Ala Leu Pro Arg Ala  
945 950 955 960

Glu Ser Asp Met Asp Ala Ala Ile Arg Ile Phe Phe Gly Glu Pro Asp  
965 970 975

Ala Gly Leu Arg Gln Arg Ile Gly Arg Arg Leu Gln Glu Val Arg Ala  
980 985 990

Tyr Ile Gly Asp Leu Ser Pro Val Asn Asp Val Leu Tyr Arg Ala Gly  
995 1000 1005

Tyr Asp Leu Asp Asp Val Ala Thr Leu Phe Asn Ala Val Asp Arg  
1010 1015 1020

Asn Thr Ser Leu Gly Arg Gln Ala Arg Met Glu Leu Tyr Leu Asp  
1025 1030 1035

Ala Ile Val Asp Leu His Ala Arg Leu Gly Tyr Glu Asn Ala Arg  
1040 1045 1050

Phe Val Asp Leu Met Ala Phe His Leu Leu Ser Leu Gly His Ala  
1055 1060 1065

Ala Thr Ala Ser Glu Val Val Glu Ala Val Ser Pro Arg Leu Leu  
1070 1075 1080

Gly Asn Val Phe Asp Ile Ser Asn Val Ala Gln Leu Glu Arg Gly  
1085 1090 1095

Ile Gly Asn Pro Ala Ser Thr Gly Leu Phe Val Met Leu Gly Ala  
1100 1105 1110

Tyr Ser Glu Ser Ser Pro Ala Ile Phe Gln Ser Phe Val Asn Asp  
1115 1120 1125

Ile Phe Pro Ala Trp Arg Gln Ala Ser Gly Gly Gly Pro Leu Val  
1130 1135 1140

Trp Asn Phe Gly Pro Ala Ala Ile Ser Pro Thr Arg Leu Asp Tyr

1145		1150		1155
Ala Asn Thr Asp Ile Gly Leu	Leu Asn His Gly Asp	Ile Ser Pro		
1160	1165	1170		
Leu Arg Ala Arg Pro Pro Leu	Gly Gly Arg Arg Asp	Ile Asp Leu		
1175	1180	1185		
Pro Pro Gly Leu Asp Ile Ser	Phe Val Arg Tyr Asp	Arg Pro Val		
1190	1195	1200		
Arg Met Ser Ala Pro Arg Ala	Leu Asp Ala Ser Val	Phe Arg Pro		
1205	1210	1215		
Val Asp Gly Pro Val His Gly	Tyr Ile Gln Ser Trp	Thr Gly Ala		
1220	1225	1230		
Glu Ile Glu Tyr Ala Tyr Gly	Ala Pro Ala Ala Ala	Arg Glu Val		
1235	1240	1245		
Met Leu Thr Asp Asn Val Arg	Ile Ile Ser Ile Glu	Asn Gly Asp		
1250	1255	1260		
Glu Gly Ala Ile Gly Val Arg	Val Arg Leu Asp Thr	Val Pro Val		
1265	1270	1275		
Ala Thr Pro Leu Ile Leu Thr	Gly Gly Ser Leu Ser	Gly Cys Thr		
1280	1285	1290		
Thr Met Val Gly Val Lys Glu	Gly Tyr Leu Ala Phe	Tyr His Thr		
1295	1300	1305		
Gly Lys Ser Thr Glu Leu Gly	Asp Trp Ala Thr Ala	Arg Glu Gly		
1310	1315	1320		
Val Gln Ala Leu Tyr Gln Ala	His Leu Ala Met Gly	Tyr Ala Pro		
1325	1330	1335		
Ile Ser Ile Pro Ala Pro Met	Arg Asn Asp Asp Leu	Val Ser Ile		
1340	1345	1350		
Ala Ala Thr Tyr Asp Arg Ala	Val Ile Ala Tyr Leu	Gly Lys Asp		
1355	1360	1365		
Val Pro Gly Gly Gly Ser Thr	Arg Ile Thr Arg His	Asp Glu Gly		
1370	1375	1380		



Ala Gly Ser Val Val Ser Phe Asp Tyr Asn Ala Ala Val Gln Ala  
1385 1390 1395

Ser Ala Val Pro Arg Leu Gly Gln Val Tyr Val Leu Ile Ser Asn  
1400 1405 1410

Asp Gly Gln Gly Ala Arg Ala Val Leu Leu Ala Glu Asp Leu Ala  
1415 1420 1425

Trp Ala Gly Ser Gly Ser Ala Leu Asp Val Leu Asn Glu Arg Leu  
1430 1435 1440

Val Thr Leu Phe Pro Ala Pro Val  
1445 1450

<210> 5  
<211> 240  
<212> PRT  
<213> Salmonella typhimurium

<400> 5

Met Thr Lys Ile Thr Leu Ser Pro Gln Asn Phe Arg Ile Gln Lys Gln  
1 5 10 15

Glu Thr Thr Leu Leu Lys Glu Lys Ser Thr Glu Lys Asn Ser Leu Ala  
20 25 30

Lys Ser Ile Leu Ala Val Lys Asn His Phe Ile Glu Leu Arg Ser Lys  
35 40 45

Leu Ser Glu Arg Phe Ile Ser His Lys Asn Thr Glu Ser Ser Ala Thr  
50 55 60

His Phe His Arg Gly Ser Ala Ser Glu Gly Arg Ala Val Leu Thr Asn  
65 70 75 80

Lys Val Val Lys Asp Phe Met Leu Gln Thr Leu Asn Asp Ile Asp Ile  
85 90 95

Arg Gly Ser Ala Ser Lys Asp Pro Ala Tyr Ala Ser Gln Thr Arg Glu  
100 105 110

Ala Ile Leu Ser Ala Val Tyr Ser Lys Asn Lys Asp Gln Cys Cys Asn  
115 120 125

Leu Leu Ile Ser Lys Gly Ile Asn Ile Ala Pro Phe Leu Gln Glu Ile  
130 135 140

Gly Glu Ala Ala Lys Asn Ala Gly Leu Pro Gly Thr Thr Lys Asn Asp  
145 150 155 160

Val Phe Thr Pro Ser Gly Ala Gly Ala Asn Pro Phe Ile Thr Pro Leu  
165 170 175

Ile Ser Ser Ala Asn Ser Lys Tyr Pro Arg Met Phe Ile Asn Gln His  
180 185 190

Gln Gln Ala Ser Phe Lys Ile Tyr Ala Glu Lys Ile Ile Met Thr Glu  
195 200 205

Val Ala Pro Leu Phe Asn Glu Cys Ala Met Pro Thr Pro Gln Gln Phe  
210 215 220

Gln Leu Ile Leu Glu Asn Ile Ala Asn Lys Tyr Ile Gln Tyr Thr Pro  
225 230 235 240

<210> 6  
<211> 240  
<212> PRT  
<213> Salmonella typhimurium

<400> 6

Met Thr Asn Ile Thr Leu Ser Thr Gln His Tyr Arg Ile His Arg Ser  
1 5 10 15

Asp Val Glu Pro Val Lys Glu Lys Thr Thr Glu Lys Asp Ile Phe Ala  
20 25 30

Lys Ser Ile Thr Ala Val Arg Asn Ser Phe Ile Ser Leu Ser Thr Ser  
35 40 45

Leu Ser Asp Arg Phe Ser Leu His Gln Gln Thr Asp Ile Pro Thr Thr  
50 55 60

His Phe His Arg Gly Asn Ala Ser Glu Gly Arg Ala Val Leu Thr Ser  
65 70 75 80

Lys Thr Val Lys Asp Phe Met Leu Gln Lys Leu Asn Ser Leu Asp Ile  
85 90 95

Lys Gly Asn Ala Ser Lys Asp Pro Ala Tyr Ala Arg Gln Thr Cys Glu  
100 105 110

Ala Ile Leu Ser Ala Val Tyr Ser Asn Asn Lys Asp Gln Cys Cys Lys  
115 120 125

Leu Leu Ile Ser Lys Gly Val Ser Ile Thr Pro Phe Leu Lys Glu Ile  
130 135 140

Gly Glu Ala Ala Gln Asn Ala Gly Leu Pro Gly Glu Ile Lys Asn Gly  
145 150 155 160

Val Phe Thr Pro Gly Gly Ala Gly Ala Asn Pro Phe Val Val Pro Leu  
165 170 175

Ile Ala Ser Ala Ser Ile Lys Tyr Pro His Met Phe Ile Asn His Asn  
180 185 190

Gln Gln Val Ser Phe Lys Ala Tyr Ala Glu Lys Ile Val Met Lys Glu  
195 200 205

Val Thr Pro Leu Phe Asn Lys Gly Thr Met Pro Thr Pro Gln Gln Phe  
210 215 220

Gln Leu Thr Ile Glu Asn Ile Ala Asn Lys Tyr Leu Gln Asn Ala Ser  
225 230 235 240

<210> 7  
<211> 166  
<212> PRT  
<213> Shigella flexneri

<400> 7

Met Glu Ile Gln Asn Thr Lys Ser Ala Pro Ile Leu Tyr Thr Asp Ile  
1 5 10 15

Ser Thr Lys Gln Thr Gln Ser Ser Ser Glu Thr Gln Lys Ser Gln Asn  
20 25 30

Tyr Gln Gln Leu Ala Ala His Ile Pro Leu Asn Val Gly Lys Asn Pro  
35 40 45

Val Leu Thr Thr Thr Leu Asn Asp Asp Gln Leu Leu Lys Leu Ser Glu  
50 55 60

Gln Val Gln His Asp Ser Glu Ile Ile Ala Arg Leu Thr Asp Lys Lys  
65 70 75 80

Met Lys Asp Leu Ser Glu Met Ser His Thr Ile Thr Pro Glu Asn Thr  
85 90 95

Leu Asp Ile Ser Ser Leu Ser Ser Asn Ala Val Ser Leu Ile Ile Ser  
100 105 110

Val Ala Val Leu Leu Ser Ala Leu Arg Thr Ala Glu Thr Arg Leu Gly  
115 120 125

Ser Gln Leu Ser Leu Ile Ala Phe Asp Ala Thr Lys Ser Ala Ala Glu  
130 135 140

Asn Ile Val Arg Gln Gly Leu Ala Ala Leu Ser Ser Ser Ile Thr Gly  
145 150 155 160

Ala Val Thr Gln Val Gly  
165

<210> 8  
<211> 1186  
<212> PRT  
<213> Helicobacter pylori

<400> 8

Met Thr Asn Glu Thr Ile Asp Gln Thr Arg Thr Pro Asp Gln Thr Gln  
1 5 10 15

Ser Gln Thr Ala Phe Asp Pro Gln Gln Phe Ile Asn Asn Leu Gln Val  
20 25 30

Ala Phe Ile Lys Val Asp Asn Val Val Ala Ser Phe Asp Pro Asp Gln  
35 40 45

Lys Pro Ile Val Asp Lys Asn Asp Arg Asp Asn Arg Gln Ala Phe Asp  
50 55 60

Gly Ile Ser Gln Leu Arg Glu Glu Tyr Ser Asn Lys Ala Ile Lys Asn  
65 70 75 80

Pro Thr Lys Lys Asn Gln Tyr Phe Ser Asp Phe Ile Asp Lys Ser Asn  
85 90 95

Asp Leu Ile Asn Lys Asp Asn Leu Ile Asp Val Glu Ser Ser Thr Lys  
100 105 110

Ser Phe Gln Lys Phe Gly Asp Gln Arg Tyr Gln Ile Phe Thr Ser Trp  
115 120 125

Val Ser His Gln Lys Asp Pro Ser Lys Ile Asn Thr Arg Ser Ile Arg  
130 135 140

Asn Phe Met Glu Asn Ile Ile Gln Pro Pro Ile Pro Asp Asp Lys Glu  
145 150 155 160

Lys Ala Glu Phe Leu Lys Ser Ala Lys Gln Ser Phe Ala Gly Ile Ile  
165 170 175

Ile Gly Asn Gln Ile Arg Thr Asp Gln Lys Phe Met Gly Val Phe Asp  
180 185 190

Glu Ser Leu Lys Glu Arg Gln Glu Ala Glu Lys Asn Gly Gly Pro Thr  
195 200 205

Gly Gly Asp Trp Leu Asp Ile Phe Leu Ser Phe Ile Phe Asn Lys Lys  
210 215 220

Gln Ser Ser Asp Val Lys Glu Ala Ile Asn Gln Glu Pro Val Pro His  
225 230 235 240

Val Gln Pro Asp Ile Ala Thr Thr Thr Thr Asp Ile Gln Gly Leu Pro  
245 250 255

Pro Glu Ala Arg Asp Leu Leu Asp Glu Arg Gly Asn Phe Ser Lys Phe  
260 265 270

Thr Leu Gly Asp Met Glu Met Leu Asp Val Glu Gly Val Ala Asp Ile  
275 280 285

Asp Pro Asn Tyr Lys Phe Asn Gln Leu Leu Ile His Asn Asn Ala Leu  
290 295 300

Ser Ser Val Leu Met Gly Ser His Asn Gly Ile Glu Pro Glu Lys Val  
305 310 315 320

Ser Leu Leu Tyr Ala Gly Asn Gly Gly Phe Gly Asp Lys His Asp Trp  
325 330 335

Asn Ala Thr Val Gly Tyr Lys Asp Gln Gln Gly Asn Asn Val Ala Thr  
340 345 350

Leu Ile Asn Val His Met Lys Asn Gly Ser Gly Leu Val Ile Ala Gly  
355 360 365

Gly Glu Lys Gly Ile Asn Asn Pro Ser Phe Tyr Leu Tyr Lys Glu Asp  
370 375 380

Gln Leu Thr Gly Ser Gln Arg Ala Leu Ser Gln Glu Glu Ile Arg Asn  
385 390 395 400

Lys Val Asp Phe Met Glu Phe Leu Ala Gln Asn Asn Thr Lys Leu Asp  
405 410 415

Asn Leu Ser Glu Lys Glu Lys Glu Lys Phe Gln Asn Glu Ile Glu Asp  
420 425 430

Phe Gln Lys Asp Ser Lys Ala Tyr Leu Asp Ala Leu Gly Asn Asp Arg  
435 440 445

Ile Ala Phe Val Ser Lys Lys Asp Thr Lys His Ser Ala Leu Ile Thr  
450 455 460

Glu Phe Asn Asn Gly Asp Leu Ser Tyr Thr Leu Lys Asp Tyr Gly Lys  
465 470 475 480

Lys Ala Asp Lys Ala Leu Asp Arg Glu Lys Asn Val Thr Leu Gln Gly  
485 490 495

Ser Leu Lys His Asp Gly Val Met Phe Val Asp Tyr Ser Asn Phe Lys  
500 505 510

Tyr Thr Asn Ala Ser Lys Asn Pro Asn Lys Gly Val Gly Ala Thr Asn  
515 520 525

Gly Val Ser His Leu Glu Ala Gly Phe Asn Lys Val Ala Val Phe Asn  
530 535 540

Leu Pro Asp Leu Asn Asn Leu Ala Ile Thr Ser Phe Val Arg Arg Asn  
545 550 555 560

Leu Glu Asn Lys Leu Thr Ala Lys Gly Leu Ser Leu Gln Glu Ala Asn  
565 570 575

Lys Leu Ile Lys Asp Phe Leu Ser Ser Asn Lys Glu Leu Ala Gly Lys  
580 585 590

Ala Leu Asn Phe Asn Lys Ala Val Ala Glu Ala Lys Ser Thr Gly Asn  
595 600 605

Tyr Asp Glu Val Lys Lys Ala Gln Lys Asp Leu Glu Lys Ser Leu Arg  
610 615 620

Lys Arg Glu His Leu Glu Lys Glu Val Glu Lys Lys Leu Glu Ser Lys  
625 630 635 640

Ser Gly Asn Lys Asn Lys Met Glu Ala Lys Ala Gln Ala Asn Ser Gln  
645 650 655

Lys Asp Glu Ile Phe Ala Leu Ile Asn Lys Glu Ala Asn Arg Asp Ala  
660 665 670

Arg Ala Ile Ala Tyr Thr Gln Asn Leu Lys Gly Ile Lys Arg Glu Leu  
675 680 685

Ser Asp Lys Leu Glu Lys Ile Ser Lys Asp Leu Lys Asp Phe Ser Lys  
690 695 700

Ser Phe Asp Glu Phe Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys Ala  
705 710 715 720

Glu Glu Thr Leu Lys Ala Leu Lys Gly Ser Val Lys Asp Leu Gly Ile  
725 730 735

Asn Pro Glu Trp Ile Ser Lys Val Glu Asn Leu Asn Ala Ala Leu Asn  
740 745 750

Glu Phe Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys Val Thr Gln Ala  
755 760 765

Lys Ser Asp Leu Glu Asn Ser Val Lys Asp Val Ile Ile Asn Gln Lys  
770 775 780

Val Thr Asp Lys Val Asp Asn Leu Asn Gln Ala Val Ser Val Ala Lys  
785 790 795 800

Ala Met Gly Asp Phe Ser Arg Val Glu Gln Val Leu Ala Asp Leu Lys  
805 810 815

Asn Phe Ser Lys Glu Gln Leu Ala Gln Gln Ala Gln Lys Asn Glu Asp  
820 825 830

Phe Asn Thr Gly Lys Asn Ser Glu Leu Tyr Gln Ser Val Lys Asn Ser  
835 840 845

Val Asn Lys Thr Leu Val Gly Asn Gly Leu Ser Gly Ile Glu Ala Thr

850

855

860

Ala Leu Ala Lys Asn Phe Ser Asp Ile Lys Lys Glu Leu Asn Glu Lys  
865 870 875 880

Phe Lys Asn Phe Asn Asn Asn Asn Asn Gly Leu Lys Asn Ser Thr Glu  
885 890 895

Pro Ile Tyr Ala Lys Val Asn Lys Lys Lys Thr Gly Gln Val Ala Ser  
900 905 910

Pro Glu Glu Pro Ile Tyr Thr Gln Val Ala Lys Lys Val Asn Ala Lys  
915 920 925

Ile Asp Arg Leu Asn Gln Ile Ala Ser Gly Leu Gly Gly Val Gly Gln  
930 935 940

Ala Ala Gly Phe Pro Leu Lys Arg His Asp Lys Val Asp Asp Leu Ser  
945 950 955 960

Lys Val Gly Leu Ser Ala Ser Pro Glu Pro Ile Tyr Ala Thr Ile Asp  
965 970 975

Asp Leu Gly Gly Pro Phe Pro Leu Lys Arg His Asp Lys Val Asp Asp  
980 985 990

Leu Ser Lys Val Gly Arg Ser Arg Asn Gln Glu Leu Ala Gln Lys Ile  
995 1000 1005

Asp Asn Leu Asn Gln Ala Val Ser Glu Ala Lys Ala Gly Phe Phe  
1010 1015 1020

Gly Asn Leu Glu Gln Thr Ile Asp Lys Leu Lys Asp Ser Thr Lys  
1025 1030 1035

Lys Asn Val Met Asn Leu Tyr Val Glu Ser Ala Lys Lys Val Pro  
1040 1045 1050

Ala Ser Leu Ser Ala Lys Leu Asp Asn Tyr Ala Ile Asn Ser His  
1055 1060 1065

Thr Arg Ile Asn Ser Asn Ile Gln Asn Gly Ala Ile Asn Glu Lys  
1070 1075 1080

Ala Thr Gly Met Leu Thr Gln Lys Asn Pro Glu Trp Leu Lys Leu  
1085 1090 1095



Val Asn Asp Lys Ile Val Ala His Asn Val Gly Ser Val Ser Leu  
1100 1105 1110

Ser Glu Tyr Asp Lys Ile Gly Phe Asn Gln Lys Asn Met Lys Asp  
1115 1120 1125

Tyr Ser Asp Ser Phe Lys Phe Ser Thr Lys Leu Asn Asn Ala Val  
1130 1135 1140

Lys Asp Ile Lys Ser Gly Phe Thr His Phe Leu Ala Asn Ala Phe  
1145 1150 1155

Ser Thr Gly Tyr Tyr Cys Leu Ala Arg Glu Asn Ala Glu His Gly  
1160 1165 1170

Ile Lys Asn Val Asn Thr Lys Gly Gly Phe Gln Lys Ser  
1175 1180 1185

<210> 9  
<211> 201  
<212> PRT  
<213> Homo sapiens

<400> 9

Ser Ser Gly Pro Ser Ser Ser Leu Asp Asn Gly Asn Ser Leu Asp Val  
1 5 10 15

Leu Lys Asn His Val Leu Asn Glu Leu Ile Gln Thr Glu Arg Val Tyr  
20 25 30

Val Arg Glu Leu Tyr Thr Val Leu Leu Gly Tyr Arg Ala Glu Met Asp  
35 40 45

Asn Pro Glu Met Phe Asp Leu Met Pro Pro Leu Leu Arg Asn Lys Lys  
50 55 60

Asp Ile Leu Phe Gly Asn Met Ala Glu Ile Tyr Glu Phe His Asn Asp  
65 70 75 80

Ile Phe Leu Ser Ser Leu Glu Asn Cys Ala His Ala Pro Glu Arg Val  
85 90 95

Gly Pro Cys Phe Leu Glu Arg Lys Asp Asp Phe Gln Met Tyr Ala Lys  
100 105 110

Tyr Cys Gln Asn Lys Pro Arg Ser Glu Thr Ile Trp Arg Lys Tyr Ser  
115 120 125

Glu Cys Ala Phe Phe Gln Glu Cys Gln Arg Lys Leu Lys His Arg Leu  
130 135 140

Arg Leu Asp Ser Tyr Leu Leu Lys Pro Val Gln Arg Ile Thr Lys Tyr  
145 150 155 160

Gln Leu Leu Leu Lys Glu Leu Leu Lys Tyr Ser Lys Asp Cys Glu Gly  
165 170 175

Ser Ala Leu Leu Lys Lys Ala Leu Asp Ala Met Leu Asp Leu Leu Lys  
180 185 190

Ser Val Asn Asp Ser Met His Gln Ile  
195 200

